18. What are the methods commonly used in computational protein structure prediction?

19. Briefly explain the concept of autocorrelation in the context of three-dimensional protein structures.

20. Evaluate the impact of advancements in computing power on the development and application of docking algorithms.

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23PEMB24A — BIOINFORMATICS

Time : Three hours   Maximum : 75 marks

SECTION A — (10 × 2 = 20 marks)

Answer ALL the questions.

1. What is the main role of a bioinformatician in present biological research area?

2. Define term database.

3. How to read phylogenetic tree?

4. Extend substitution matrices.

5. Which force filed should be used for energy minimization of homology model?

6. List out the two computational methods commonly used for predicting protein.

7. Outline of ligand components.

8. Explain the significance of SAR in toxicity of compounds.

9. What is molecular docking?

10. What is drug discovering?

SECTION B — (5 × 5 = 25 marks)

Answer ALL the questions.

11. (a) Describe about Data Visualization.

Or

(b) Determine the biological primary and derided data bases.

12. (a) What is Character based tree reconstruction?

Or

(b) Explain how consensus trees are generated and their role the reliability of phylogenetic.

13. (a) Explore the applications of 3D prediction in protein.

Or

(b) Draw a Structure of alignment its comparison.

14. (a) Determine the Properties of ligand compounds.

Or

(b) Analyze the different types of computational methods and algorithms used for predicting compound toxicity.

15. (a) Explore the use of data mining and machine learning techniques in immuno informatics research.

Or

(b) Define molecular docking and its importance in drug discovery. How does molecular docking software facilitate this process?

SECTION C — (3 × 10 = 30 marks)

Answer any THREE questions.

16. Discuss the process of data curation and its significance in maintaining high-quality biological data.

17. Compare the difference between distance and character-based methods for constructing phylogenetic trees.